

## Publication

Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of chlorite dismutase: a detoxifying enzyme producing molecular oxygen

### JournalArticle (Originalarbeit in einer wissenschaftlichen Zeitschrift)

**ID** 4530728

**Author(s)** de Geus, Daniël C.; Thomassen, Ellen A. J.; van der Feltz, Clarisse L.; Abrahams, Jan Pieter

**Author(s) at UniBasel** [Abrahams, Jan Pieter](#) ;

**Year** 2008

**Title** Cloning, expression, purification, crystallization and preliminary X-ray diffraction analysis of chlorite dismutase: a detoxifying enzyme producing molecular oxygen

**Journal** Acta Crystallographica Section F

**Volume** 64

**Number** Pt 8

**Pages / Article-Number** 730-2

**Mesh terms** Science & TechnologyLife Sciences & BiomedicinePhysical SciencesBiochemical Research MethodsBiochemistry & Molecular BiologyBiophysicsCrystallographyBiochemistry & Molecular Biology-BiophysicsCrystallography

Chlorite dismutase, a homotetrameric haem-based protein, is one of the key enzymes of (per) chlorate-reducing bacteria. It is highly active ( $>2 \text{ kU mg}^{-1}$ ) in reducing the toxic compound chlorite to the innocuous chloride anion and molecular oxygen. Chlorite itself is produced as the intermediate product of (per) chlorate reduction. The chlorite dismutase gene in *Azospira oryzae* strain GR-1 employing degenerate primers has been identified and the active enzyme was subsequently overexpressed in *Escherichia coli*. Chlorite dismutase was purified, proven to be active and crystallized using sitting drops with PEG 2000 MME, KSCN and ammonium sulfate as precipitants. The crystals belonged to space group  $P2(1)2(1)2$  and were most likely to contain six subunits in the asymmetric unit. The refined unit-cell parameters were  $a = 164.46$ ,  $b = 169.34$ ,  $c = 60.79$  angstrom. The crystals diffracted X-rays to 2.1 angstrom resolution on a synchrotron radiation source and a three-wavelength MAD data set has been collected. Determination of the chlorite dismutase structure will provide insights into the active site of the enzyme, for which no structures are currently available.

**Publisher** Wiley

**ISSN/ISBN** 1744-3091 ; 2053-230X

**edoc-URL** <https://edoc.unibas.ch/75847/>

**Full Text on edoc** No;

**Digital Object Identifier DOI** 10.1107/S1744309108020551

**PubMed ID** <http://www.ncbi.nlm.nih.gov/pubmed/18678943>

**ISI-Number** 000258071000013

**Document type (ISI)** Journal Article